Diseases Caused by Bacteria and Phytoplasmas

First Report of *Pectobacterium aroidearum* Causing Soft Rot in Olecranon Honey Peach (*Prunus persica*) in China

Zhibin Liang,^{1,2} Huidi Liu,^{1,2} Zeling Xu,¹ and Lian-Hui Zhang^{1,2,†}

¹ Guangdong Province Key Laboratory of Microbial Signals and Disease Control, Integrative Microbiology Research Centre, South China Agricultural University, Guangzhou 510642, China

² Guangdong Laboratory for Lingnan Modern Agriculture, Guangzhou 510642, China

Funding: This study was supported by the KeyRealm R&D Program of Guangdong Province (2018B020205003 and 2020B020209001), Basic and Applied Basic Research Foundation of Guangdong Province (2020A1515110465), and National Natural Science Foundation of China (32000085). Plant Dis. 106:1746, 2022; published online as <https://doi.org/10.1094/PDIS-10-21-2238-PDN>. Accepted for publication 23 November 2021.

Olecranon honey peach (*Prunus persica* L.) is a popular fruit tree cultivated in Guangdong Province, China. Due to its excellent economic value and popularity, it has been widely planted in several other southern provinces and autonomous regions in China, including Yunnan, Hunan, Jiangxi, Guizhou, and Guangxi. In Lianping County of Guangdong Province alone, annual fruit production was about 78,800 metric tons (Xie et al. 2017). In July 2021, fruits showing soft rot symptoms were collected from an olecranon honey peach plantation in Lechang, Guangdong. Symptoms included tissue disintegration with bacterial oozes and rotting smells. To isolate the causal agent of soft rot, bacterial oozes from rotted fruits were streaked on a modified YEB agar plate (Huang et al. 2021), and 21 bacterial colonies were selected for PCR amplification using primers targeting the conserved region of the 16S rDNA gene (Wei et al. 2020). A BLASTn analysis of the DNA sequences of the obtained PCR fragments on the NCBI website indicated that 17 isolates named as ZL strains were potential species of *Pectobacterium* with about 99% similarity (GenBank accession no. of ZL1: OK189602) to *Pectobacterium aroidearum* SCRI 109^T (GenBank accession no. NR_159926). Three isolates (ZL1, ZL2, and ZL3) were selected for an assay of pathogenicity. Bacterial suspensions (10 µl, 1×10^6 CFU/ml) of the isolates were injected into olecranon honey peach fruits using a syringe. Some fruits were similarly injected with sterile distilled water as the negative control. After 18 h of incubation at 25°C, the typical symptom of soft rot (i.e., tissue decay) was visible on the fruits inoculated with the suspensions. After inoculation for 42 h, bacterial oozes exuded from rotting tissues. Peach fruits without injuries were also sprayed with the suspensions under the same

conditions, but decay symptoms were not observed, suggesting that bacterial infection needs wounding or injuries. To fulfill Koch's postulates, bacterial colonies were reisolated from oozes, and the conserved region of 16S rDNA fragments was amplified and sequenced. Bioinformatics analysis of the DNA sequence data confirmed that all the isolated colonies were *Pectobacterium* strains. Using the Biolog Gen III system, representative strain ZL1 was identified as *Pectobacterium* (SIM 0.56). Transmission electron microscopy analysis showed that cells of ZL1 were rod-shaped with peripheral flagella. To further determine the species of ZL strains, eight housekeeping genes (*acnA*, *gapA*, *icd*, *mdh*, *mtlD*, *pgi*, *proA*, and *rpoS*) were analyzed by the methods described previously (Nabhan et al. 2013). The amplified DNA sequences analyzed by the BLASTn program in NCBI showed that the sequences of the eight genes from strains ZL1, ZL2, and ZL3 were identical to each other (GenBank accession nos. OK274248 to OK274255), and most of the gene sequences shared over 99% similarity to their counterparts in *P. aroidearum* L6 (GenBank accession no. NZ_CP065044) (Xu et al. 2021), except that the *acnA* and *proA* genes showed about 98% and 96% similarity, respectively, to the corresponding genes of *P. aroidearum* L6. In addition, a multilocus sequence analysis using DNA sequences of the eight genes showed that ZL strains were grouped with other *P. aroidearum* strains. Taken together, the molecular and biochemical assays confirmed that the ZL strains were *P. aroidearum*. To our knowledge, this is the first report of *P. aroidearum* causing soft rot disease in olecranon honey peach in China. *P. aroidearum* is a relatively newly described soft rot pathogen (Nabhan et al. 2013). More recently, the pathogen was found causing soft rot infections in lettuce, Chinese cabbage, pepper (*Capsicum annuum*) fruits, konjac, carrot, and *Syngonium podophyllum* (Barroso et al. 2019; Moraes et al. 2020; Sun et al. 2019; Tang et al. 2021; Xu et al. 2021). The results of this study add a new plant species to the host range of *P. aroidearum*.

References:

- Barroso, K. A., et al. 2019. Plant Dis. 103:3274.
- Huang, S., et al. 2021. Plant Dis. 105:3737.
- Moraes, A. J. G., et al. 2020. Plant Dis. 104:3054.
- Nabhan, S., et al. 2013. Int. J. Syst. Evol. Microbiol. 63:2520.
- Sun, M., et al. 2019. Int. J. Mol. Sci. 20:1937.
- Tang, W. Q., et al. 2021. Plant Dis. 105:695.
- Wei, H. Y., et al. 2020. Plant Dis. 104:969.
- Xie, C. G., et al. 2017. Agric. Dev. Equip. 2:2 (In Chinese).
- Xu, P., et al. 2021. Front. Microbiol. 12:679102.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: olecranon honey peach, *Pectobacterium aroidearum*, soft rot disease

[†]Indicates the corresponding author.
L. H. Zhang; lhzhang01@scau.edu.cn